

10 Rec 106 JAN 2003

SEQUENCE LISTING

<110> MALLET , Francois

COSSET , Francois-loic

BLOND , Jean-Luc

LAVILLETTE , Dimitri

BOUTON , Olivier

RUGGIERI , Alessia

<120> Method for detecting the expression of an envelope protein of a human endogenous retrovirus and uses of a gene coding for said protein

<130> 112062

<140> 10/069,883

<141> 2002-05-01

<150> PCT/FR00/02429

<151> 2000-09-01

<150> FR-9911141

<151> 1999-09-01

<150> FR-9911793

<151> 1999-09-15

<160> 64

<170> PatentIn version 3.1

<210> 1

<211> 538

<212> PRT

<213> Homo sapiens

<400> 1

Met Ala Leu Pro Tyr His Ile Phe Leu Phe Thr Val Leu Leu Pro Ser
1 5 10 15

Phe Thr Leu Thr Ala Pro Pro Pro Cys Arg Cys Met Thr Ser Ser Ser
20 25 30

Pro Tyr Gln Glu Phe Leu Trp Arg Met Gln Arg Pro Gly Asn Ile Asp
35 40 45

Ala Pro Ser Tyr Arg Ser Leu Ser Lys Gly Thr Pro Thr Phe Thr Ala
50 55 60

His Thr His Met Pro Arg Asn Cys Tyr His Ser Ala Thr Leu Cys Met
65 70 75 80

His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys
85 90 95

Pro Gly Gly Leu Gly Val Thr Val Cys Trp Thr Tyr Phe Thr Gln Thr
100 105 110

Gly Met Ser Asp Gly Gly Gly Val Gln Asp Gln Ala Arg Glu Lys His
115 120 125

Val Lys Glu Val Ile Ser Gln Leu Thr Arg Val His Gly Thr Ser Ser
130 135 140

Pro Tyr Lys Gly Leu Asp Leu Ser Lys Leu His Glu Thr Leu Arg Thr
145 150 155 160

His Thr Arg Leu Val Ser Leu Phe Asn Thr Thr Leu Thr Gly Leu His
165 170 175

Glu Val Ser Ala Gln Asn Pro Thr Asn Cys Trp Ile Cys Leu Pro Leu
180 185 190

Asn Phe Arg Pro Tyr Val Ser Ile Pro Val Pro Glu Gln Trp Asn Asn
195 200 205

Phe Ser Thr Glu Ile Asn Thr Thr Ser Val Leu Val Gly Pro Leu Val
 210 215 220

Ser Asn Leu Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe
 225 230 235 240

Ser Asn Thr Thr Tyr Thr Thr Asn Ser Gln Cys Ile Arg Trp Val Thr
 245 250 255

Pro Pro Thr Gln Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys
 260 265 270

Gly Thr Ser Ala Tyr Arg Cys Leu Asn Gly Ser Ser Glu Ser Met Cys
 275 280 285

Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp
 290 295 300

Leu Tyr Ser Tyr Val Ile Ser Lys Pro Arg Asn Lys Arg Val Pro Ile
 305 310 315 320

Leu Pro Phe Val Ile Gly Ala Gly Val Leu Gly Ala Leu Gly Thr Gly
 325 330 335

Ile Gly Gly Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln
 340 345 350

Glu Leu Asn Gly Asp Met Glu Arg Val Ala Asp Ser Leu Val Thr Leu
 355 360 365

Gln Asp Gln Leu Asn Ser Leu Ala Ala Val Val Leu Gln Asn Arg Arg
 370 375 380

Ala Leu Asp Leu Leu Thr Ala Glu Arg Gly Gly Thr Cys Leu Phe Leu
 385 390 395 400

Gly Glu Glu Cys Cys Tyr Tyr Val Asn Gln Ser Gly Ile Val Thr Glu
 405 410 415

Lys Val Lys Glu Ile Arg Asp Arg Ile Gln Arg Arg Ala Glu Glu Leu
 420 425 430

Arg Asn Thr Gly Pro Trp Gly Leu Leu Ser Gln Trp Met Pro Trp Ile
 435 440 445

Leu Pro Phe Leu Gly Pro Leu Ala Ala Ile Ile Leu Leu Leu Leu Phe
 450 455 460

Gly Pro Cys Ile Phe Asn Leu Leu Val Asn Phe Val Ser Ser Arg Ile
 465 470 475 480

Glu Ala Val Lys Leu Gln Met Glu Pro Lys Met Gln Ser Lys Thr Lys
 485 490 495

Ile Tyr Arg Arg Pro Leu Asp Arg Pro Ala Ser Pro Arg Ser Asp Val
 500 505 510

Asn Asp Ile Lys Gly Thr Pro Pro Glu Glu Ile Ser Ala Ala Gln Pro
 515 520 525

Leu Leu Arg Pro Asn Ser Ala Gly Ser Ser
 530 535

<210> 2

<211> 2781

<212> DNA

<213> Homo sapiens

<400> 2

atgggagctg ttttcatgct atttactctt attaaatctt gcaactgcac tcttctggtc	60
catgtttctt acggctcgag ctgagctttt gctcaccgtc caccactgct gtttgccacc	120
accgcagacc tgccgctgac tcccatccct ctggatcctg cagggtgtcc gctgtgctcc	180
tgatccagcg aggcgcccat tgccgctccc aattgggcta aaggcttgcc attgttcctg	240
cacggctaag tgcttgggtt tgttctaatt gagctgaaca ctagtcaactg ggttccatgg	300
ttctcttctg tgaccacagg cttctaatag aactataaca cttaccacat ggcccaagat	360
tccattcctt ggaatccgtg aggccaagaa ctccaggtca gagaatacga ggcttgccac	420
catcttgga gggcctgct accatcttgg aagtgggtca ccaccatctt gggagctctg	480
tgagcaagga cccccggta acattttggc aaccacgaac ggacatccaa agtgatacat	540
cctgggaagg accctacca gtcattttat ctacccaac tgcggttaaa gtggctggag	600
tggagtcttg gatacatcac acttgagtca aatcctggat actgccaaag gaacctgaaa	660
atccaggaga caacgctagc tattcctgtg aacctctaga ggatttgccg ctgctcttca	720
aacaacaacc aggaggaaag taactaaaat cataaatccc catggccctc ccttatcata	780

tttttctctt tactgttctt ttaccctctt tcaactctcac tgcacccccct ccatgcccgt	840
gtatgaccag tagctcccct taccaagagt ttctatggag aatgcagcgt cccggaaata	900
ttgatgcccc atcgtatagg agtctttcta agggaacccc caccttcaact gccacacccc	960
atatgccccg caactgctat cactctgccca ctctttgcat gcatgcaaact actcattatt	1020
ggacaggaaa aatgattaat cctagttgtc ctggaggact tggagtcact gtctgttgga	1080
cttacttcac ccaaactggt atgtctgatg ggggtggagt tcaagatcag gcaagagaaa	1140
aacatgtaaa agaagtaatc tcccaactca cccgggtaca tggcacctct agcccctaca	1200
aaggactaga tctctcaaaa ctacatgaaa ccctcogtac ccatactcgc ctggtaagcc	1260
tatttaatac caccctcaact gggctccatg aggtctcggc ccaaaaccct actaactgtt	1320
ggatatgcct cccctgaac ttcaggccat atgtttcaat ccctgtacct gaacaatgga	1380
acaacttcag cacagaaata aacaccactt ccgttttagt aggacctctt gttccaatc	1440
tggaaataac ccatacctca aacctcacct gtgtaaaatt tagcaatact acatacacia	1500
ccaactccca atgcatcagg tgggtaactc ctccacaca aatagtctgc ctaccctcag	1560
gaatattttt tgtctgtggt acctcagcct atcgttggtt gaatggctct tcagaatcta	1620
tgtgcttctt ctcatcttta gtgcccccta tgaccatcta cactgaacaa gatttataca	1680
gttatgtcat atctaagccc cgcaacaaaa gagtaccat tcttcctttt gttataggag	1740
cgggagtgcct aggtgcacta ggtactggca ttggcggtat cacaacctct actcagttct	1800
actacaaact atctcaagaa ctaaattggg acatggaacg ggtcgccgac tccctggtca	1860
ccttgcaaga tcagcttaac tccctagcag cagtagtcct tcaaaatcga agagctttag	1920
acttgctaac cgctgaaaga gggggaacct gtttattttt aggggaagaa tgctgttatt	1980
atgttaatca atccggaatc gtcactgaga aagttaaaga aattcgagat cgaatacaac	2040
gtagagcaga ggagcttcga aacactggac cctggggcct cctcagccaa tggatgccct	2100
ggattctccc cttcttagga cctctagcag ctataatatt gctactcctc tttggaccct	2160
gtatctttta cctccttggt aactttgtct cttccagaat cgaagctgta aaactacaaa	2220
tggagcccaa gatgcagtcc aagactaaga tctaccgcag acccctggac cggcctgcta	2280
gccacgatac tgatgttaat gacatcaaag gcacccctcc tgaggaaatc tcagctgcac	2340
aacctctact acgcccgaat tcagcaggaa gcagttagag cggtcgtcgg ccaacctccc	2400
caacagcact taggttttcc tgttgagatg ggggactgag agacaggact agctggattt	2460
cctaggctga ctaagaatcc ctaagcctag ctgggaaggt gaccacatcc acctttaaac	2520
acggggcttg caacttagct cacacctgac caatcagaga gctcactaaa atgctaatta	2580
ggcaaagaca ggaggtaaag aaatagccaa tcctctattg cctgagagca cagcaggagg	2640

gacaatgatac gggatataaa cccaagtctt cgagccggca acggcaaccc cctttgggtc 2700
ccctcccttt gtatgggagc tctgttttca tgctatttca ctctattaaa tcttgcaact 2760
gcaaaaaaaaa aaaaaaaaaa a 2781

<210> 3

<211> 28

<212> DNA

<213> Homo sapiens

<400> 3
caaaacgcct ggagatacag caattatc 28

<210> 4

<211> 25

<212> DNA

<213> Homo sapiens

<400> 4
gcaccctcat ggttgtgtta cttgg 25

<210> 5

<211> 26

<212> DNA

<213> Homo sapiens

<400> 5
ctgaaaatcc aggagacaac gctagc 26

<210> 6

<211> 25

<212> DNA

<213> Homo sapiens

<400> 6

25

gcaccctcat ggttggtgta cttgg

<210> 7

<211> 36

<212> DNA

<213> Homo sapiens

<400> 7
ttggtaccca aaacgcctgg agatacagca attatc

36

<210> 8

<211> 29

<212> DNA

<213> Homo sapiens

<400> 8
aactcgagtg aaatagcatg aaaacagag

29

<210> 9

<211> 25

<212> DNA

<213> Homo sapiens

<400> 9
aggaaagtaa ctaaaatcat aaatc

25

<210> 10

<211> 20

<212> DNA

<213> Homo sapiens

<400> 10
ggttcctta gaaagactcc

20

<210> 11

<211> 22

<212> DNA

<213> Homo sapiens

<400> 11
aatattgatg ccccatcgta ta

22

<210> 12

<211> 21

<212> DNA

<213> Homo sapiens

<400> 12
ccagtttggg tgaagtaagt c

21

<210> 13

<211> 21

<212> DNA

<213> Homo sapiens

<400> 13
ggaggacttg gagtcactgt c

21

<210> 14

<211> 20

<212> DNA

<213> Homo sapiens

<400> 14
aggcgagtat gggtacggag

20

<210> 15

<211> 23

<212> DNA

<213> Homo sapiens

<400> 15
ggactagatc tctcaaaact aca

23

<210> 16

<211> 22

<212> DNA

<213> Homo sapiens

<400> 16
acggaagtgg tgtttatttc tg

22

<210> 17

<211> 21

<212> DNA

<213> Homo sapiens

<400> 17
cctgaacaat ggaacaactt c

21

<210> 18

<211> 20

<212> DNA

<213> Homo sapiens

<400> 18
attcctgagg gtaggcagac

20

<210> 19

<211> 20

<212> DNA

<213> Homo sapiens

<400> 19

ggtaactcct cccacacaaa

20

<210> 20

<211> 21

<212> DNA

<213> Homo sapiens

<400> 20

gaatgggtac ttttttggtg c

21

<210> 21

<211> 23

<212> DNA

<213> Homo sapiens

<400> 21

tacagttatg tcatatctaa gcc

23

<210> 22

<211> 22

<212> DNA

<213> Homo sapiens

<400> 22

taagttgatc ttgcaagggtg ac

22

<210> 23

<211> 20

<212> DNA

<213> Homo sapiens

<400> 23

ctaaatgggg acatggaacg

20

<210> 24

<211> 24

<212> DNA

<213> Homo sapiens

<400> 24
tattcgatct ggaatttctt caac

24

<210> 25

<211> 20

<212> DNA

<213> Homo sapiens

<400> 25
caatccggaa tcgtcactga

20

<210> 26

<211> 23

<212> DNA

<213> Homo sapiens

<400> 26
agacaaagtt aacaaggagg ttc

23

<210> 27

<211> 22

<212> DNA

<213> Homo sapiens

<400> 27
actcctcttt ggaccctgta tc

22

<210> 28

<211> 18

<212> DNA

<213> Homo sapiens

<400> 28
gaggttgcc gaccaccg

18

<210> 29

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> primer U6198

<400> 29
caaacgcct ggagatacag caattatc

28

<210> 30

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> primer L6186

<400> 30
gcaccctcat ggttgtgtta cttgg

25

<210> 31

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> primer U6189

<400> 31
ctgaaaatcc aggagacaac gctagc

26

<210> 32

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> primer U6460

<400> 32

ttggtaccca aaacgcctgg agatacagca attatc

36

<210> 33

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> primer L5643

<400> 33

aactcgagtg aaatagcatg aaaacagag

29

<210> 34

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> primer U6302

<400> 34

aggaaagtaa ctaaaatcat aaatc

25

<210> 35

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> primer L6303

<400> 35
ggttccctta gaaagactcc

20

<210> 36

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> primer U6304

<400> 36
aatattgatg ccccatcgta ta

22

<210> 37

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> primer L6305

<400> 37
ccagtttggg tgaagtaagt c

21

<210> 38

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> primer U6306

<400> 38
ggaggacttg gagtcactgt c

21

<210> 39

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> primer L6307

<400> 39
aggcgagtat gggtagcgag

20

<210> 40

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> primer U6308

<400> 40
ggactagatc tctcaaaact aca

23

<210> 41

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> primer L6309

<400> 41
acggaagtgg tgtttatttc tg

22

<210> 42

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> primer U6310

<400> 42

cctgaacaat ggaacaactt c

21

<210> 43

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> primer L6311

<400> 43

attcctgagg gtaggcagac

20

<210> 44

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> primer U6312

<400> 44

ggtaactcct cccacacaaa

20

<210> 45

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> primer L6313

<400> 45
gaatgggtac tcttttggtg c

21

<210> 46

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> primer U6314

<400> 46
tacagttatg tcatatctaa gcc

23

<210> 47

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> primer L6315

<400> 47
taagttgatc ttgcaaggtg ac

22

<210> 48

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> primer U6316

<400> 48

ctaaatgggg acatggaacg

20

<210> 49

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> primer L6317

<400> 49
tattcgatct ggaatttctt caac

24

<210> 50

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> primer U6318

<400> 50
caatccggaa tcgtcactga

20

<210> 51

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> primer L6319

<400> 51
agacaaagtt aacaaggagg ttc

23

<210> 52

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> primer U6320

<400> 52
actcctcttt ggaccctgta tc

22

<210> 53

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> primer L6321

<400> 53
gaggttg gcc gaccaccg

18

<210> 54

<211> 1617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1614)

<223>

<400> 54
atg gcc ctc cct tat cat att ttt ctc ttt act gtt ctt tta ccc tct
Met Ala Leu Pro Tyr His Ile Phe Leu Phe Thr Val Leu Leu Pro Ser
1 5 10 15

48

ttc act ctc act gca ccc cct cca tgc cgc tgt atg acc agt agc tcc
Phe Thr Leu Thr Ala Pro Pro Pro Cys Arg Cys Met Thr Ser Ser Ser
20 25 30

96

cct tac caa gag ttt cta tgg aga atg cag cgt ccc gga aat att gat	144
Pro Tyr Gln Glu Phe Leu Trp Arg Met Gln Arg Pro Gly Asn Ile Asp	
35 40 45	
gcc cca tgc tat agg agt ctt tct aag gga acc ccc acc ttc act gcc	192
Ala Pro Cys Tyr Arg Ser Leu Ser Lys Gly Thr Pro Thr Phe Thr Ala	
50 55 60	
cac acc cat atg ccc cgc aac tgc tat cac tct gcc act ctt tgc atg	240
His Thr His Met Pro Arg Asn Cys Tyr His Ser Ala Thr Leu Cys Met	
65 70 75 80	
cat gca aat act cat tat tgg aca gga aaa atg att aat cct agt tgt	288
His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys	
85 90 95	
cct gga gga ctt gga gtc act gtc tgt tgg act tac ttc acc caa act	336
Pro Gly Gly Leu Gly Val Thr Val Cys Trp Thr Tyr Phe Thr Gln Thr	
100 105 110	
ggt atg tct gat ggg ggt gga gtt caa gat cag gca aga gaa aaa cat	384
Gly Met Ser Asp Gly Gly Gly Val Gln Asp Gln Ala Arg Glu Lys His	
115 120 125	
gaa aaa gaa gta atc tcc caa ctc acc cgg gta cat ggc acc tct agc	432
Xaa Lys Glu Val Ile Ser Gln Leu Thr Arg Val His Gly Thr Ser Ser	
130 135 140	
ccc tac aaa gga cta gat ctc tca aaa cta cat gaa acc ctc cgt acc	480
Pro Tyr Lys Gly Leu Asp Leu Ser Lys Leu His Glu Thr Leu Arg Thr	
145 150 155 160	
cat act cgc ctg gta agc cta ttt aat acc acc ctc act ggg ctc cat	528
His Thr Arg Leu Val Ser Leu Phe Asn Thr Thr Leu Thr Gly Leu His	
165 170 175	
gag gtc tcg gcc caa aac cct act aac tgt tgg ata tgc ctc ccc ctg	576
Glu Val Ser Ala Gln Asn Pro Thr Asn Cys Trp Ile Cys Leu Pro Leu	
180 185 190	
aac ttc agg cca tat gtt tca atc cct gta cct gaa caa tgg aac aac	624
Asn Phe Arg Pro Tyr Val Ser Ile Pro Val Pro Glu Gln Trp Asn Asn	
195 200 205	
ttc agc aca gaa ata aac acc act tcc gtt tta gta gga cct ctt gyt	672
Phe Ser Thr Glu Ile Asn Thr Thr Ser Val Leu Val Gly Pro Leu Xaa	
210 215 220	
tcc aat ctg gaa ata acc cat acc tca aac ctc acc tgt gta aaa ttt	720
Ser Asn Leu Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe	
225 230 235 240	
agc aat act aca tac aca acc aac tcc caa tgc atc agg tgg gta act	768
Ser Asn Thr Thr Tyr Thr Thr Asn Ser Gln Cys Ile Arg Trp Val Thr	
245 250 255	
cct ccc aca caa ata gtc tgc cta ccc tca gga ata ttt ttt gtc tgt	816
Pro Pro Thr Gln Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys	
260 265 270	

ggt acc tca gcc tat cgt tgt ttg aat ggc tct tca gaa tct atg tgc	864
Gly Thr Ser Ala Tyr Arg Cys Leu Asn Gly Ser Ser Glu Ser Met Cys	
275 280 285	
ttc ctc tca ttc tta gtg ccc cct atg acc atc tac act gaa caa gat	912
Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp	
290 295 300	
tta tac art tat gtc ata tct aag ccc cgc aac aaa aga gta ccc att	960
Leu Tyr Xaa Tyr Val Ile Ser Lys Pro Arg Asn Lys Arg Val Pro Ile	
305 310 315 320	
ctt cct ttt gtt ata gga gca gga gtg cta ggt gca cta ggt act ggc	1008
Leu Pro Phe Val Ile Gly Ala Gly Val Leu Gly Ala Leu Gly Thr Gly	
325 330 335	
att ggc ggt atc aca acc tct act cag ttc tac tac aaa cta tct caa	1056
Ile Gly Gly Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln	
340 345 350	
gaa cta aat ggg gac atg gaa cgg gtc gcc gac tcc ctg gtc acc ttg	1104
Glu Leu Asn Gly Asp Met Glu Arg Val Ala Asp Ser Leu Val Thr Leu	
355 360 365	
caa gat caa ctt aac tcc cta gcg aca gta gtc ctt caa aat cga aga	1152
Gln Asp Gln Leu Asn Ser Leu Ala Thr Val Val Leu Gln Asn Arg Arg	
370 375 380	
gct tta gac ttg cta acc gct gaa aga ggg gga acc tgt tta ttt tta	1200
Ala Leu Asp Leu Leu Thr Ala Glu Arg Gly Gly Thr Cys Leu Phe Leu	
385 390 395 400	
ggg gaa gaa tgc tgt tat tat gtt aat caa tcc gga atc gtc act gag	1248
Gly Glu Glu Cys Cys Tyr Tyr Val Asn Gln Ser Gly Ile Val Thr Glu	
405 410 415	
aaa gtt aaa gaa att cga gat cga ata caa cgt aga gca gag gag ctt	1296
Lys Val Lys Glu Ile Arg Asp Arg Ile Gln Arg Arg Ala Glu Glu Leu	
420 425 430	
cga aac act gga ccc tgg ggc ctc ctc agc caa tgg atg ccc tgg att	1344
Arg Asn Thr Gly Pro Trp Gly Leu Leu Ser Gln Trp Met Pro Trp Ile	
435 440 445	
ctc ccc ttc tta gga cct cta gca gct ata ata ttg cta ctc ctc ttt	1392
Leu Pro Phe Leu Gly Pro Leu Ala Ala Ile Ile Leu Leu Leu Phe	
450 455 460	
gga ccc tgt atc ttt aac ctc ctt gtt aac ttt gtc tct tcc aga atc	1440
Gly Pro Cys Ile Phe Asn Leu Leu Val Asn Phe Val Ser Ser Arg Ile	
465 470 475 480	
gaa gct gta aaa cta caa atg gag ccc aag atg cag tcc aag act aag	1488
Glu Ala Val Lys Leu Gln Met Glu Pro Lys Met Gln Ser Lys Thr Lys	
485 490 495	
atc tac cgc aga ccc ctg gac cgg aat gct agc cca cga tct gat gtt	1536
Ile Tyr Arg Arg Pro Leu Asp Arg Asn Ala Ser Pro Arg Ser Asp Val	
500 505 510	

cta cta cgc ccc aat tca gca gga agc agt tag 1617
Leu Leu Arg Pro Asn Ser Ala Gly Ser Ser
530 535

<213> Homo sapiens

<400> 55

Ala Pro Cys Tyr Arg Ser Leu Ser Lys Gly Thr Pro Thr Phe Thr Ala
50 55 60 .

His Thr His Met Pro Arg Asn Cys Tyr His Ser Ala Thr Leu Cys Met
65 70 75 80

His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys
85 90 95

Pro Gly Gly Leu Gly Val Thr Val Cys Trp Thr Tyr Phe Thr Gln Thr
100 105 110

Gly Met Ser Asp Gly Gly Gly Val Gln Asp Gln Ala Arg Glu Lys His
115 120 125

Xaa Lys Glu Val Ile Ser Gln Leu Thr Arg Val His Gly Thr Ser Ser
130 135 140

Pro Tyr Lys Gly Leu Asp Leu Ser Lys Leu His Glu Thr Leu Arg Thr
145 150 155 160

His Thr Arg Leu Val Ser Leu Phe Asn Thr Thr Leu Thr Gly Leu His
165 170 175

Glu Val Ser Ala Gln Asn Pro Thr Asn Cys Trp Ile Cys Leu Pro Leu
180 185 190

Asn Phe Arg Pro Tyr Val Ser Ile Pro Val Pro Glu Gln Trp Asn Asn
195 200 205

Phe Ser Thr Glu Ile Asn Thr Thr Ser Val Leu Val Gly Pro Leu Xaa
210 215 220

Ser Asn Leu Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe
225 230 235 240

Ser Asn Thr Thr Tyr Thr Thr Asn Ser Gln Cys Ile Arg Trp Val Thr
245 250 255

Pro Pro Thr Gln Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys
260 265 270

Gly Thr Ser Ala Tyr Arg Cys Leu Asn Gly Ser Ser Glu Ser Met Cys
275 280 285

Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp
290 295 300

Leu Tyr Xaa Tyr Val Ile Ser Lys Pro Arg Asn Lys Arg Val Pro Ile
 305 310 315 320

Leu Pro Phe Val Ile Gly Ala Gly Val Leu Gly Ala Leu Gly Thr Gly
 325 330 335

Ile Gly Gly Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln
 340 345 350

Glu Leu Asn Gly Asp Met Glu Arg Val Ala Asp Ser Leu Val Thr Leu
 355 360 365

Gln Asp Gln Leu Asn Ser Leu Ala Thr Val Val Leu Gln Asn Arg Arg
 370 375 380

Ala Leu Asp Leu Leu Thr Ala Glu Arg Gly Gly Thr Cys Leu Phe Leu
 385 390 395 400

Gly Glu Glu Cys Cys Tyr Tyr Val Asn Gln Ser Gly Ile Val Thr Glu
 405 410 415

Lys Val Lys Glu Ile Arg Asp Arg Ile Gln Arg Arg Ala Glu Glu Leu
 420 425 430

Arg Asn Thr Gly Pro Trp Gly Leu Leu Ser Gln Trp Met Pro Trp Ile
 435 440 445

Leu Pro Phe Leu Gly Pro Leu Ala Ala Ile Ile Leu Leu Leu Phe
 450 455 460

Gly Pro Cys Ile Phe Asn Leu Leu Val Asn Phe Val Ser Ser Arg Ile
 465 470 475 480

Glu Ala Val Lys Leu Gln Met Glu Pro Lys Met Gln Ser Lys Thr Lys
 485 490 495

Ile Tyr Arg Arg Pro Leu Asp Arg Asn Ala Ser Pro Arg Ser Asp Val
 500 505 510

Asn Asp Ile Lys Gly Thr Pro Pro Glu Glu Ile Ser Ala Ala Gln Pro
 515 520 525

Leu Leu Arg Pro Asn Ser Ala Gly Ser Ser
 530 535

<210> 56
 <211> 1617
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1614)
 <223>

<400> 56		
atg gcc ctc cct tat cat att ttt ctc ttt act gtt ctt tta ccc tct		48
Met Ala Leu Pro Tyr His Ile Phe Leu Phe Thr Val Leu Leu Pro Ser		
1 5 10 15		
ttc act ctc act gca ccc cct cca tgc cgc tgt atg acc agt agc tcc		96
Phe Thr Leu Thr Ala Pro Pro Pro Cys Arg Cys Met Thr Ser Ser Ser		
20 25 30		
cct tac caa gag ttt cta tgg aga atg cag cgt ccc gga aat att gat		144
Pro Tyr Gln Glu Phe Leu Trp Arg Met Gln Arg Pro Gly Asn Ile Asp		
35 40 45		
gcc cca tgc tat agg agt ctt tct aag gga acc ccc acc ttc act gcc		192
Ala Pro Cys Tyr Arg Ser Leu Ser Lys Gly Thr Pro Thr Phe Thr Ala		
50 55 60		
cac acc cat atg ccc cgc aac tgc tat cac tct gcc act ctt tgc atg		240
His Thr His Met Pro Arg Asn Cys Tyr His Ser Ala Thr Leu Cys Met		
65 70 75 80		
cat gca aat act cat tat tgg aca gga aaa atg att aat cct agt tgt		288
His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys		
85 90 95		
cct gga gga ctt gga gtc act gtc tgt tgg act tac ttc acc caa act		336
Pro Gly Gly Leu Gly Val Thr Val Cys Trp Thr Tyr Phe Thr Gln Thr		
100 105 110		
ggt atg tct gat ggg ggt gga gtt caa gat cag gca aga gaa aaa cat		384
Gly Met Ser Asp Gly Gly Gly Val Gln Asp Gln Ala Arg Glu Lys His		
115 120 125		
gta aaa gaa gta atc tcc caa ctc acc cgg gta cat ggc acc tct agc		432
Val Lys Glu Val Ile Ser Gln Leu Thr Arg Val His Gly Thr Ser Ser		
130 135 140		
ccc tac aaa gga cta gat ctc tca aaa cta cat gaa acc ctc cgt acc		480
Pro Tyr Lys Gly Leu Asp Leu Ser Lys Leu His Glu Thr Leu Arg Thr		
145 150 155 160		

cat act cgc ctg gta agc cta ttt aat acc acc ctc act ggg ctc cat	528
His Thr Arg Leu Val Ser Leu Phe Asn Thr Thr Leu Thr Gly Leu His	
165 170 175	
gag gtc tcg gcc caa aac cct act aac tgt tgg ata tgc ctc ccc ctg	576
Glu Val Ser Ala Gln Asn Pro Thr Asn Cys Trp Ile Cys Leu Pro Leu	
180 185 190	
aac ttc agg cca tat gtt tca atc cct gta cct gaa caa tgg aac aac	624
Asn Phe Arg Pro Tyr Val Ser Ile Pro Val Pro Glu Gln Trp Asn Asn	
195 200 205	
ttc agc aca gaa ata aac acc act tcc gtt tta gta gga cct ctt gtt	672
Phe Ser Thr Glu Ile Asn Thr Thr Ser Val Leu Val Gly Pro Leu Val	
210 215 220	
tcc aat ctg gaa ata acc cat acc tca aac ctc acc tgt gta aaa ttt	720
Ser Asn Leu Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe	
225 230 235 240	
agc aat act aca tac aca acc aac tcc caa tgc atc agg tgg gta act	768
Ser Asn Thr Thr Tyr Thr Thr Asn Ser Gln Cys Ile Arg Trp Val Thr	
245 250 255	
cct ccc aca caa ata gtc tgc cta ccc tca gga ata ttt ttt gtc tgt	816
Pro Pro Thr Gln Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys	
260 265 270	
ggg acc tca gcc tat cgt tgt ttg aat ggc tct tca gaa tct atg tgc	864
Gly Thr Ser Ala Tyr Arg Cys Leu Asn Gly Ser Ser Glu Ser Met Cys	
275 280 285	
ttc ctc tca ttc tta gtg ccc cct atg acc atc tac act gaa caa gat	912
Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp	
290 295 300	
tta tac agt tat gtc ata tct aag ccc cgc aac aaa aga gta ccc att	960
Leu Tyr Ser Tyr Val Ile Ser Lys Pro Arg Asn Lys Arg Val Pro Ile	
305 310 315 320	
ctt cct ttt gtt ata gga gca gga gtg cta ggt gca cta ggt act ggc	1008
Leu Pro Phe Val Ile Gly Ala Gly Val Leu Gly Ala Leu Gly Thr Gly	
325 330 335	
att ggc ggt atc aca acc tct act cag ttc tac tac aaa cta tct caa	1056
Ile Gly Gly Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln	
340 345 350	
gaa cta aat ggg gac atg gaa cgg gtc gcc gac tcc ctg gtc acc ttg	1104
Glu Leu Asn Gly Asp Met Glu Arg Val Ala Asp Ser Leu Val Thr Leu	
355 360 365	
caa gat caa ctt aac tcc cta gcg aca gta gtc ctt caa aat cga aga	1152
Gln Asp Gln Leu Asn Ser Leu Ala Thr Val Val Leu Gln Asn Arg Arg	
370 375 380	
gct tta gac ttg cta acc gct gaa aga ggg gga acc tgt tta ttt tta	1200
Ala Leu Asp Leu Leu Thr Ala Glu Arg Gly Gly Thr Cys Leu Phe Leu	
385 390 395 400	

ggg gaa gaa tgc tgt tat tat gtt aat caa tcc gga atc gtc act gag 1248
 Gly Glu Glu Cys Tyr Tyr Val Asn Gln Ser Gly Ile Val Thr Glu
 405 410 415
 aaa gtt aaa gaa att cga gat cga ata caa cgt aga gca gag gag ctt 1296
 Lys Val Lys Glu Ile Arg Asp Arg Ile Gln Arg Arg Ala Glu Glu Leu
 420 425 430
 cga aac act gga ccc tgg ggc ctc ctc agc caa tgg atg ccc tgg att 1344
 Arg Asn Thr Gly Pro Trp Gly Leu Leu Ser Gln Trp Met Pro Trp Ile
 435 440 445
 ctc ccc ttc tta gga cct cta gca gct ata ata ttg cta ctc ctc ttt 1392
 Leu Pro Phe Leu Gly Pro Leu Ala Ala Ile Ile Leu Leu Leu Phe
 450 455 460
 gga ccc tgt atc ttt aac ctc ctt gtt aac ttt gtc tct tcc aga atc 1440
 Gly Pro Cys Ile Phe Asn Leu Leu Val Asn Phe Val Ser Ser Arg Ile
 465 470 475 480
 gaa gct gta aaa cta caa atg gag ccc aag atg cag tcc aag act aag 1488
 Glu Ala Val Lys Leu Gln Met Glu Pro Lys Met Gln Ser Lys Thr Lys
 485 490 495
 atc tac cgc aga ccc ctg gac cgg aat gct agc cca cga tct gat gtt 1536
 Ile Tyr Arg Arg Pro Leu Asp Arg Asn Ala Ser Pro Arg Ser Asp Val
 500 505 510
 aat gac atc aaa ggc acc cct cct gag gaa atc tca gct gca caa cct 1584
 Asn Asp Ile Lys Gly Thr Pro Pro Glu Glu Ile Ser Ala Ala Gln Pro
 515 520 525
 cta cta cgc ccc aat tca gca gga agc agt tag 1617
 Leu Leu Arg Pro Asn Ser Ala Gly Ser Ser
 530 535

<210> 57

<211> 538

<212> PRT

<213> Homo sapiens

<400> 57

Met Ala Leu Pro Tyr His Ile Phe Leu Phe Thr Val Leu Leu Pro Ser
 1 5 10 15

Phe Thr Leu Thr Ala Pro Pro Pro Cys Arg Cys Met Thr Ser Ser Ser
 20 25 30

Pro Tyr Gln Glu Phe Leu Trp Arg Met Gln Arg Pro Gly Asn Ile Asp
 35 40 45

Ala Pro Cys Tyr Arg Ser Leu Ser Lys Gly Thr Pro Thr Phe Thr Ala
50 55 60

His Thr His Met Pro Arg Asn Cys Tyr His Ser Ala Thr Leu Cys Met
65 70 75 80

His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys
85 90 95

Pro Gly Gly Leu Gly Val Thr Val Cys Trp Thr Tyr Phe Thr Gln Thr
100 105 110

Gly Met Ser Asp Gly Gly Gly Val Gln Asp Gln Ala Arg Glu Lys His
115 120 125

Val Lys Glu Val Ile Ser Gln Leu Thr Arg Val His Gly Thr Ser Ser
130 135 140

Pro Tyr Lys Gly Leu Asp Leu Ser Lys Leu His Glu Thr Leu Arg Thr
145 150 155 160

His Thr Arg Leu Val Ser Leu Phe Asn Thr Thr Leu Thr Gly Leu His
165 170 175

Glu Val Ser Ala Gln Asn Pro Thr Asn Cys Trp Ile Cys Leu Pro Leu
180 185 190

Asn Phe Arg Pro Tyr Val Ser Ile Pro Val Pro Glu Gln Trp Asn Asn
195 200 205

Phe Ser Thr Glu Ile Asn Thr Thr Ser Val Leu Val Gly Pro Leu Val
210 215 220

Ser Asn Leu Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe
225 230 235 240

Ser Asn Thr Thr Tyr Thr Thr Asn Ser Gln Cys Ile Arg Trp Val Thr
245 250 255

Pro Pro Thr Gln Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys
260 265 270

Gly Thr Ser Ala Tyr Arg Cys Leu Asn Gly Ser Ser Glu Ser Met Cys
275 280 285

Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp
 290 295 300

Leu Tyr Ser Tyr Val Ile Ser Lys Pro Arg Asn Lys Arg Val Pro Ile
 305 310 315 320

Leu Pro Phe Val Ile Gly Ala Gly Val Leu Gly Ala Leu Gly Thr Gly
 325 330 335

Ile Gly Gly Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln
 340 345 350

Glu Leu Asn Gly Asp Met Glu Arg Val Ala Asp Ser Leu Val Thr Leu
 355 360 365

Gln Asp Gln Leu Asn Ser Leu Ala Thr Val Val Leu Gln Asn Arg Arg
 370 375 380

Ala Leu Asp Leu Leu Thr Ala Glu Arg Gly Gly Thr Cys Leu Phe Leu
 385 390 395 400

Gly Glu Glu Cys Cys Tyr Tyr Val Asn Gln Ser Gly Ile Val Thr Glu
 405 410 415

Lys Val Lys Glu Ile Arg Asp Arg Ile Gln Arg Arg Ala Glu Glu Leu
 420 425 430

Arg Asn Thr Gly Pro Trp Gly Leu Leu Ser Gln Trp Met Pro Trp Ile
 435 440 445

Leu Pro Phe Leu Gly Pro Leu Ala Ala Ile Ile Leu Leu Leu Leu Phe
 450 455 460

Gly Pro Cys Ile Phe Asn Leu Leu Val Asn Phe Val Ser Ser Arg Ile
 465 470 475 480

Glu Ala Val Lys Leu Gln Met Glu Pro Lys Met Gln Ser Lys Thr Lys
 485 490 495

Ile Tyr Arg Arg Pro Leu Asp Arg Asn Ala Ser Pro Arg Ser Asp Val
 500 505 510

Asn Asp Ile Lys Gly Thr Pro Pro Glu Glu Ile Ser Ala Ala Gln Pro
 515 520 525

Leu Leu Arg Pro Asn Ser Ala Gly Ser Ser
530 535

<210> 58

<211> 1617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1614)

<223>

<400> 58	
atg gcc ctc cct tat cat att ttt ctc ttt act gtt ctt tta ccc tct	48
Met Ala Leu Pro Tyr His Ile Phe Leu Phe Thr Val Leu Leu Pro Ser	
1 5 10 15	
ttc act ctc act gca ccc cct cca tgc cgc tgt atg acc agt agc tcc	96
Phe Thr Leu Thr Ala Pro Pro Pro Cys Arg Cys Met Thr Ser Ser Ser	
20 25 30	
cct tac caa gag ttt cta tgg aga atg cag cgt ccc gga aat att gat	144
Pro Tyr Gln Glu Phe Leu Trp Arg Met Gln Arg Pro Gly Asn Ile Asp	
35 40 45	
gcc cca tgc tat agg agt ctt tct aag gga acc ccc acc ttc act gcc	192
Ala Pro Cys Tyr Arg Ser Leu Ser Lys Gly Thr Pro Thr Phe Thr Ala	
50 55 60	
cac acc cat atg ccc cgc aac tgc tat cac tct gcc act ctt tgc atg	240
His Thr His Met Pro Arg Asn Cys Tyr His Ser Ala Thr Leu Cys Met	
65 70 75 80	
cat gca aat act cat tat tgg aca gga aaa atg att aat cct agt tgt	288
His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys	
85 90 95	
cct gga gga ctt gga gtc act gtc tgt tgg act tac ttc acc caa act	336
Pro Gly Gly Leu Gly Val Thr Val Cys Trp Thr Tyr Phe Thr Gln Thr	
100 105 110	
ggt atg tct gat ggg ggt gga gtt caa gat cag gca aga gaa aaa cat	384
Gly Met Ser Asp Gly Gly Gly Val Gln Asp Gln Ala Arg Glu Lys His	
115 120 125	
gta aaa gaa gta atc tcc caa ctc acc cgg gta cat ggc acc tct agc	432
Val Lys Glu Val Ile Ser Gln Leu Thr Arg Val His Gly Thr Ser Ser	
130 135 140	

ccc tac aaa gga cta gat ctc tca aaa cta cat gaa acc ctc cgt acc	480
Pro Tyr Lys Gly Leu Asp Leu Ser Lys Leu His Glu Thr Leu Arg Thr	
145 150 155 160	
cat act cgc ctg gta agc cta ttt aat acc acc ctc act ggg ctc cat	528
His Thr Arg Leu Val Ser Leu Phe Asn Thr Thr Leu Thr Gly Leu His	
165 170 175	
gag gtc tcg gcc caa aac cct act aac tgt tgg ata tgc ctc ccc ctg	576
Glu Val Ser Ala Gln Asn Pro Thr Asn Cys Trp Ile Cys Leu Pro Leu	
180 185 190	
aac ttc agg cca tat gtt tca atc cct gta cct gaa caa tgg aac aac	624
Asn Phe Arg Pro Tyr Val Ser Ile Pro Val Pro Glu Gln Trp Asn Asn	
195 200 205	
ttc agc aca gaa ata aac acc act tcc gtt tta gta gga cct ctt gct	672
Phe Ser Thr Glu Ile Asn Thr Thr Ser Val Leu Val Gly Pro Leu Ala	
210 215 220	
tcc aat ctg gaa ata acc cat acc tca aac ctc acc tgt gta aaa ttt	720
Ser Asn Leu Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe	
225 230 235 240	
agc aat act aca tac aca acc aac tcc caa tgc atc agg tgg gta act	768
Ser Asn Thr Thr Tyr Thr Thr Asn Ser Gln Cys Ile Arg Trp Val Thr	
245 250 255	
cct ccc aca caa ata gtc tgc cta ccc tca gga ata ttt ttt gtc tgt	816
Pro Pro Thr Gln Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys	
260 265 270	
ggt acc tca gcc tat cgt tgt ttg aat ggc tct tca gaa tct atg tgc	864
Gly Thr Ser Ala Tyr Arg Cys Leu Asn Gly Ser Ser Glu Ser Met Cys	
275 280 285	
ttc ctc tca ttc tta gtg ccc cct atg acc atc tac act gaa caa gat	912
Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp	
290 295 300	
tta tac aat tat gtc ata tct aag ccc cgc aac aaa aga gta ccc att	960
Leu Tyr Asn Tyr Val Ile Ser Lys Pro Arg Asn Lys Arg Val Pro Ile	
305 310 315 320	
ctt cct ttt gtt ata gga gca gga gtg cta ggt gca cta ggt act ggc	1008
Leu Pro Phe Val Ile Gly Ala Gly Val Leu Gly Ala Leu Gly Thr Gly	
325 330 335	
att ggc ggt atc aca acc tct act cag ttc tac tac aaa cta tct caa	1056
Ile Gly Gly Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln	
340 345 350	
gaa cta aat ggg gac atg gaa cgg gtc gcc gac tcc ctg gtc acc ttg	1104
Glu Leu Asn Gly Asp Met Glu Arg Val Ala Asp Ser Leu Val Thr Leu	
355 360 365	
caa gat caa ctt aac tcc cta gcg aca gta gtc ctt caa aat cga aga	1152
Gln Asp Gln Leu Asn Ser Leu Ala Thr Val Val Leu Gln Asn Arg Arg	
370 375 380	

gct tta gac ttg cta acc gct gaa aga ggg gga acc tgt tta ttt tta 1200
 Ala Leu Asp Leu Leu Thr Ala Glu Arg Gly Gly Thr Cys Leu Phe Leu
 385 390 395 400
 ggg gaa gaa tgc tgt tat tat gtt aat caa tcc gga atc gtc act gag 1248
 Gly Glu Glu Cys Cys Tyr Tyr Val Asn Gln Ser Gly Ile Val Thr Glu
 405 410 415
 aaa gtt aaa gaa att cga gat cga ata caa cgt aga gca gag gag ctt 1296
 Lys Val Lys Glu Ile Arg Asp Arg Ile Gln Arg Arg Ala Glu Glu Leu
 420 425 430
 cga aac act gga ccc tgg ggc ctc ctc agc caa tgg atg ccc tgg att 1344
 Arg Asn Thr Gly Pro Trp Gly Leu Leu Ser Gln Trp Met Pro Trp Ile
 435 440 445
 ctc ccc ttc tta gga cct cta gca gct ata ata ttg cta ctc ctc ttt 1392
 Leu Pro Phe Leu Gly Pro Leu Ala Ala Ile Ile Leu Leu Leu Leu Phe
 450 455 460
 gga ccc tgt atc ttt aac ctc ctt gtt aac ttt gtc tct tcc aga atc 1440
 Gly Pro Cys Ile Phe Asn Leu Leu Val Asn Phe Val Ser Ser Arg Ile
 465 470 475 480
 gaa gct gta aaa cta caa atg gag ccc aag atg cag tcc aag act aag 1488
 Glu Ala Val Lys Leu Gln Met Glu Pro Lys Met Gln Ser Lys Thr Lys
 485 490 495
 atc tac cgc aga ccc ctg gac cgg aat gct agc cca cga tct gat gtt 1536
 Ile Tyr Arg Arg Pro Leu Asp Arg Asn Ala Ser Pro Arg Ser Asp Val
 500 505 510
 aat gac atc aaa ggc acc cct cct gag gaa atc tca gct gca caa cct 1584
 Asn Asp Ile Lys Gly Thr Pro Pro Glu Glu Ile Ser Ala Ala Gln Pro
 515 520 525
 cta cta cgc ccc aat tca gca gga agc agt tag 1617
 Leu Leu Arg Pro Asn Ser Ala Gly Ser Ser
 530 535

<210> 59

<211> 538

<212> PRT

<213> Homo sapiens

<400> 59

Met Ala Leu Pro Tyr His Ile Phe Leu Phe Thr Val Leu Leu Pro Ser
 1 5 10 15

Phe Thr Leu Thr Ala Pro Pro Pro Cys Arg Cys Met Thr Ser Ser Ser
 20 25 30

Pro Tyr Gln Glu Phe Leu Trp Arg Met Gln Arg Pro Gly Asn Ile Asp
 35 40 45

Ala Pro Cys Tyr Arg Ser Leu Ser Lys Gly Thr Pro Thr Phe Thr Ala
 50 55 60

His Thr His Met Pro Arg Asn Cys Tyr His Ser Ala Thr Leu Cys Met
 65 70 75 80

His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys
 85 90 95

Pro Gly Gly Leu Gly Val Thr Val Cys Trp Thr Tyr Phe Thr Gln Thr
 100 105 110

Gly Met Ser Asp Gly Gly Gly Val Gln Asp Gln Ala Arg Glu Lys His
 115 120 125

Val Lys Glu Val Ile Ser Gln Leu Thr Arg Val His Gly Thr Ser Ser
 130 135 140

Pro Tyr Lys Gly Leu Asp Leu Ser Lys Leu His Glu Thr Leu Arg Thr
 145 150 155 160

His Thr Arg Leu Val Ser Leu Phe Asn Thr Thr Leu Thr Gly Leu His
 165 170 175

Glu Val Ser Ala Gln Asn Pro Thr Asn Cys Trp Ile Cys Leu Pro Leu
 180 185 190

Asn Phe Arg Pro Tyr Val Ser Ile Pro Val Pro Glu Gln Trp Asn Asn
 195 200 205

Phe Ser Thr Glu Ile Asn Thr Thr Ser Val Leu Val Gly Pro Leu Ala
 210 215 220

Ser Asn Leu Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe
 225 230 235 240

Ser Asn Thr Thr Tyr Thr Thr Asn Ser Gln Cys Ile Arg Trp Val Thr
 245 250 255

Pro Pro Thr Gln Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys
 260 265 270

Gly Thr Ser Ala Tyr Arg Cys Leu Asn Gly Ser Ser Glu Ser Met Cys
 275 280 285

Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp
 290 295 300

Leu Tyr Asn Tyr Val Ile Ser Lys Pro Arg Asn Lys Arg Val Pro Ile
 305 310 315 320

Leu Pro Phe Val Ile Gly Ala Gly Val Leu Gly Ala Leu Gly Thr Gly
 325 330 335

Ile Gly Gly Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln
 340 345 350

Glu Leu Asn Gly Asp Met Glu Arg Val Ala Asp Ser Leu Val Thr Leu
 355 360 365

Gln Asp Gln Leu Asn Ser Leu Ala Thr Val Val Leu Gln Asn Arg Arg
 370 375 380

Ala Leu Asp Leu Leu Thr Ala Glu Arg Gly Gly Thr Cys Leu Phe Leu
 385 390 395 400

Gly Glu Glu Cys Cys Tyr Tyr Val Asn Gln Ser Gly Ile Val Thr Glu
 405 410 415

Lys Val Lys Glu Ile Arg Asp Arg Ile Gln Arg Arg Ala Glu Glu Leu
 420 425 430

Arg Asn Thr Gly Pro Trp Gly Leu Leu Ser Gln Trp Met Pro Trp Ile
 435 440 445

Leu Pro Phe Leu Gly Pro Leu Ala Ala Ile Ile Leu Leu Leu Phe
 450 455 460

Gly Pro Cys Ile Phe Asn Leu Leu Val Asn Phe Val Ser Ser Arg Ile
 465 470 475 480

Glu Ala Val Lys Leu Gln Met Glu Pro Lys Met Gln Ser Lys Thr Lys
 485 490 495

Ile Tyr Arg Arg Pro Leu Asp Arg Asn Ala Ser Pro Arg Ser Asp Val
 500 505 510

Asn Asp Ile Lys Gly Thr Pro Pro Glu Glu Ile Ser Ala Ala Gln Pro
 515 520 525

Leu Leu Arg Pro Asn Ser Ala Gly Ser Ser
 530 535

<210> 60

<211> 1617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1614)

<223>

<400> 60

atg gcc ctc cct tat cat att ttt ctc ttt act gtt ctt tta ccc tct	48
Met Ala Leu Pro Tyr His Ile Phe Leu Phe Thr Val Leu Leu Pro Ser	
1 5 10 15	

ttc act ctc act gca ccc cct cca tgc cgc tgt atg acc agt agc tcc	96
Phe Thr Leu Thr Ala Pro Pro Pro Cys Arg Cys Met Thr Ser Ser Ser	
20 25 30	

cct tac caa gag ttt cta tgg aga atg cag cgt ccc gga aat att gat	144
Pro Tyr Gln Glu Phe Leu Trp Arg Met Gln Arg Pro Gly Asn Ile Asp	
35 40 45	

gcc cca tgc tat agg agt ctt tct aag gga acc ccc acc ttc act gcc	192
Ala Pro Cys Tyr Arg Ser Leu Ser Lys Gly Thr Pro Thr Phe Thr Ala	
50 55 60	

cac acc cat atg ccc cgc aac tgc tat cac tct gcc act ctt tgc atg	240
His Thr His Met Pro Arg Asn Cys Tyr His Ser Ala Thr Leu Cys Met	
65 70 75 80	

cat gca aat act cat tat tgg aca gga aaa atg att aat cct agt tgt	288
His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys	
85 90 95	

cct gga gga ctt gga gtc act gtc tgt tgg act tac ttc acc caa act	336
Pro Gly Gly Leu Gly Val Thr Val Cys Trp Thr Tyr Phe Thr Gln Thr	
100 105 110	

ggg atg tct gat ggg ggt gga gtt caa gat cag gca aga gaa aaa cat	384
Gly Met Ser Asp Gly Gly Gly Val Gln Asp Gln Ala Arg Glu Lys His	
115 120 125	

gca aaa gaa gta atc tcc caa ctc acc cgg gta cat ggc acc tct agc	432
Ala Lys Glu Val Ile Ser Gln Leu Thr Arg Val His Gly Thr Ser Ser	
130 135 140	
ccc tac aaa gga cta gat ctc tca aaa cta cat gaa acc ctc cgt acc	480
Pro Tyr Lys Gly Leu Asp Leu Ser Lys Leu His Glu Thr Leu Arg Thr	
145 150 155 160	
cat act cgc ctg gta agc cta ttt aat acc acc ctc act ggg ctc cat	528
His Thr Arg Leu Val Ser Leu Phe Asn Thr Thr Leu Thr Gly Leu His	
165 170 175	
gag gtc tcg gcc caa aac cct act aac tgt tgg ata tgc ctc ccc ctg	576
Glu Val Ser Ala Gln Asn Pro Thr Asn Cys Trp Ile Cys Leu Pro Leu	
180 185 190	
aac ttc agg cca tat gtt tca atc cct gta cct gaa caa tgg aac aac	624
Asn Phe Arg Pro Tyr Val Ser Ile Pro Val Pro Glu Gln Trp Asn Asn	
195 200 205	
ttc agc aca gaa ata aac acc act tcc gtt tta gta gga cct ctt gtt	672
Phe Ser Thr Glu Ile Asn Thr Thr Ser Val Leu Val Gly Pro Leu Val	
210 215 220	
tcc aat ctg gaa ata acc cat acc tca aac ctc acc tgt gta aaa ttt	720
Ser Asn Leu Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe	
225 230 235 240	
agc aat act aca tac aca acc aac tcc caa tgc atc agg tgg gta act	768
Ser Asn Thr Thr Tyr Thr Thr Asn Ser Gln Cys Ile Arg Trp Val Thr	
245 250 255	
cct ccc aca caa ata gtc tgc cta ccc tca gga ata ttt ttt gtc tgt	816
Pro Pro Thr Gln Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys	
260 265 270	
ggg acc tca gcc tat cgt tgt ttg aat ggc tct tca gaa tct atg tgc	864
Gly Thr Ser Ala Tyr Arg Cys Leu Asn Gly Ser Ser Glu Ser Met Cys	
275 280 285	
ttc ctc tca ttc tta gtg ccc cct atg acc atc tac act gaa caa gat	912
Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp	
290 295 300	
tta tac agt tat gtc ata tct aag ccc cgc aac aaa aga gta ccc att	960
Leu Tyr Ser Tyr Val Ile Ser Lys Pro Arg Asn Lys Arg Val Pro Ile	
305 310 315 320	
ctt cct ttt gtt ata gga gca gga gtg cta ggt gca cta ggt act ggc	1008
Leu Pro Phe Val Ile Gly Ala Gly Val Leu Gly Ala Leu Gly Thr Gly	
325 330 335	
att ggc ggt atc aca acc tct act cag ttc tac tac aaa cta tct caa	1056
Ile Gly Gly Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln	
340 345 350	
gaa cta aat ggg gac atg gaa cgg gtc gcc gac tcc ctg gtc acc ttg	1104
Glu Leu Asn Gly Asp Met Glu Arg Val Ala Asp Ser Leu Val Thr Leu	
355 360 365	

caa gat caa ctt aac tcc cta gcg aca gta gtc ctt caa aat cga aga 1152
 Gln Asp Gln Leu Asn Ser Leu Ala Thr Val Val Leu Gln Asn Arg Arg
 370 375 380

 gct tta gac ttg cta acc gct gaa aga ggg gga acc tgt tta ttt tta 1200
 Ala Leu Asp Leu Leu Thr Ala Glu Arg Gly Gly Thr Cys Leu Phe Leu
 385 390 395 400

 ggg gaa gaa tgc tgt tat tat gtt aat caa tcc gga atc gtc act gag 1248
 Gly Glu Glu Cys Cys Tyr Tyr Val Asn Gln Ser Gly Ile Val Thr Glu
 405 410 415

 aaa gtt aaa gaa att cga gat cga ata caa cgt aga gca gag gag ctt 1296
 Lys Val Lys Glu Ile Arg Asp Arg Ile Gln Arg Arg Ala Glu Glu Leu
 420 425 430

 cga aac act gga ccc tgg ggc ctc ctc agc caa tgg atg ccc tgg att 1344
 Arg Asn Thr Gly Pro Trp Gly Leu Leu Ser Gln Trp Met Pro Trp Ile
 435 440 445

 ctc ccc ttc tta gga cct cta gca gct ata ata ttg cta ctc ctc ttt 1392
 Leu Pro Phe Leu Gly Pro Leu Ala Ala Ile Ile Leu Leu Leu Phe
 450 455 460

 gga ccc tgt atc ttt aac ctc ctt gtt aac ttt gtc tct tcc aga atc 1440
 Gly Pro Cys Ile Phe Asn Leu Leu Val Asn Phe Val Ser Ser Arg Ile
 465 470 475 480

 gaa gct gta aaa cta caa atg gag ccc aag atg cag tcc aag act aag 1488
 Glu Ala Val Lys Leu Gln Met Glu Pro Lys Met Gln Ser Lys Thr Lys
 485 490 495

 atc tac cgc aga ccc ctg gac cgg aat gct agc cca cga tct gat gtt 1536
 Ile Tyr Arg Arg Pro Leu Asp Arg Asn Ala Ser Pro Arg Ser Asp Val
 500 505 510

 aat gac atc aaa ggc acc cct cct gag gaa atc tca gct gca caa cct 1584
 Asn Asp Ile Lys Gly Thr Pro Pro Glu Glu Ile Ser Ala Ala Gln Pro
 515 520 525

 cta cta cgc ccc aat tca gca gga agc agt tag 1617
 Leu Leu Arg Pro Asn Ser Ala Gly Ser Ser
 530 535

<210> 61

<211> 538

<212> PRT

<213> Homo sapiens

<400> 61

Met Ala Leu Pro Tyr His Ile Phe Leu Phe Thr Val Leu Leu Pro Ser
 1 5 10 15

Phe Thr Leu Thr Ala Pro Pro Pro Cys Arg Cys Met Thr Ser Ser Ser
20 25 30

Pro Tyr Gln Glu Phe Leu Trp Arg Met Gln Arg Pro Gly Asn Ile Asp
35 40 45

Ala Pro Cys Tyr Arg Ser Leu Ser Lys Gly Thr Pro Thr Phe Thr Ala
50 55 60

His Thr His Met Pro Arg Asn Cys Tyr His Ser Ala Thr Leu Cys Met
65 70 75 80

His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys
85 90 95

Pro Gly Gly Leu Gly Val Thr Val Cys Trp Thr Tyr Phe Thr Gln Thr
100 105 110

Gly Met Ser Asp Gly Gly Gly Val Gln Asp Gln Ala Arg Glu Lys His
115 120 125

Ala Lys Glu Val Ile Ser Gln Leu Thr Arg Val His Gly Thr Ser Ser
130 135 140

Pro Tyr Lys Gly Leu Asp Leu Ser Lys Leu His Glu Thr Leu Arg Thr
145 150 155 160

His Thr Arg Leu Val Ser Leu Phe Asn Thr Thr Leu Thr Gly Leu His
165 170 175

Glu Val Ser Ala Gln Asn Pro Thr Asn Cys Trp Ile Cys Leu Pro Leu
180 185 190

Asn Phe Arg Pro Tyr Val Ser Ile Pro Val Pro Glu Gln Trp Asn Asn
195 200 205

Phe Ser Thr Glu Ile Asn Thr Thr Ser Val Leu Val Gly Pro Leu Val
210 215 220

Ser Asn Leu Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe
225 230 235 240

Ser Asn Thr Thr Tyr Thr Thr Asn Ser Gln Cys Ile Arg Trp Val Thr
245 250 255

Pro Pro Thr Gln Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys
260 265 270

Gly Thr Ser Ala Tyr Arg Cys Leu Asn Gly Ser Ser Glu Ser Met Cys
275 280 285

Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp
290 295 300

Leu Tyr Ser Tyr Val Ile Ser Lys Pro Arg Asn Lys Arg Val Pro Ile
305 310 315 320

Leu Pro Phe Val Ile Gly Ala Gly Val Leu Gly Ala Leu Gly Thr Gly
325 330 335

Ile Gly Gly Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln
340 345 350

Glu Leu Asn Gly Asp Met Glu Arg Val Ala Asp Ser Leu Val Thr Leu
355 360 365

Gln Asp Gln Leu Asn Ser Leu Ala Thr Val Val Leu Gln Asn Arg Arg
370 375 380

Ala Leu Asp Leu Leu Thr Ala Glu Arg Gly Gly Thr Cys Leu Phe Leu
385 390 395 400

Gly Glu Glu Cys Cys Tyr Tyr Val Asn Gln Ser Gly Ile Val Thr Glu
405 410 415

Lys Val Lys Glu Ile Arg Asp Arg Ile Gln Arg Arg Ala Glu Glu Leu
420 425 430

Arg Asn Thr Gly Pro Trp Gly Leu Leu Ser Gln Trp Met Pro Trp Ile
435 440 445

Leu Pro Phe Leu Gly Pro Leu Ala Ala Ile Ile Leu Leu Leu Leu Phe
450 455 460

Gly Pro Cys Ile Phe Asn Leu Leu Val Asn Phe Val Ser Ser Arg Ile
465 470 475 480

Glu Ala Val Lys Leu Gln Met Glu Pro Lys Met Gln Ser Lys Thr Lys
485 490 495

Ile Tyr Arg Arg Pro Leu Asp Arg Asn Ala Ser Pro Arg Ser Asp Val
 500 505 510

Asn Asp Ile Lys Gly Thr Pro Pro Glu Glu Ile Ser Ala Ala Gln Pro
 515 520 525

Leu Leu Arg Pro Asn Ser Ala Gly Ser Ser
 530 535

<210> 62

<211> 246

<212> DNA

<213> Homo sapiens

<400> 62
 tgagagacag gactagctgg atttcctagg ccgactaaga atccctaagc ctagctggga 60
 argtgaccac gtccaccttt aaacacgggg cttgcaactt agtcacacc tgaccaatca 120
 gagagctcac taaaatgcta attaggcaaa gacrggaggt aaagaaatag ccaatcatct 180
 attgcctgag agcacagcag gagggacaay ratcgggata taaaccarg ymttcgagcy 240
 ggcaac 246

<210> 63

<211> 246

<212> DNA

<213> Homo sapiens

<400> 63
 tgagagacag gactagctgg atttcctagg ccgactaaga atccctaagc ctagctggga 60
 aggtgaccac gtccaccttt aaacacgggg cttgcaactt agtcacacc tgaccaatca 120
 gagagctcac taaaatgcta attaggcaaa gacaggaggt aaagaaatag ccaatcatct 180
 attgcctgag agcacagcag gagggacaat gatcgggata taaaccaag tcttcgagcc 240
 ggcaac 246

<210> 64

<211> 246

<212> DNA

<213> Homo sapiens

<400> 64

tgagagacag gactagctgg atttcctagg ccgactaaga atccctaagc ctagctggga 60
aagtgaccac gtccaccttt aaacacgggg cttgcaactt agtcacacc tgaccaatca 120
gagagctcac taaaatgcta attaggcaaa gacgggaggt aaagaaatag ccaatcatct 180
attgcctgag agcacagcag gagggacaac aatcgggata taaaccagg cattcgagct 240
ggcaac 246

